

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Mack, David H.
- (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
EXPRESSION COMPARISON
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/020,743
(B) FILING DATE: 09-FEB-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Liebeschuetz, Joe
(B) REGISTRATION NUMBER: 37,505
(C) REFERENCE/DOCKET NUMBER: 018547034800US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 326-2400
(B) TELEFAX: (650) 326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT	60
CATGGCTGAG TGAGCCTCCC CTGGGCCAG CACCCACCT CAGCATGGTC CAAGCCCATG	120
GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC	180
CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG	240
TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA	300
CACCCCGGGA GGTCACCCTA CACTTTCTGC GCACTGCTGG ACACCCCTT ACCCGCTGGG	360
CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT	420
CAAACCTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATAACA	480
AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG	540
ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA	600
TTGCCACCCA GGGCCCCATG CCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG	660
AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC	720
ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA	780
AAGAGTGCCC AGAATACTACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT	840
CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC	900
CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC	960
CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA	1020
TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC	1080
TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA	1140
CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT	1200
CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA	1260
AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG	1320
CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG	1380
CATTTATGAC AGACAAAGAA AGAAGCCAG GTGTCTCTGGT GTTCTCTGAG ACACTCTTTG	1440
TGAGCTTCAG TTTCCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA	1500
GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG	1560
TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCAAGC ACAGGCCAGA TGCAAGAATG	1620
GGGAAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA	1680

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CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC 1740
 CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG 1800
 AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC 1860
 CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT 1920
 TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT 1980
 GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG 2040
 ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT 2100
 CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG 2160
 CCACACCTCA GGATTCTCC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA 2220
 TGAAGGTAAG ATGCCGCATC ACCAGGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT 2280
 CTCTGTGGAA ACCCCCGAGG AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC 2340
 TTCTCTCCTG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT 2400
 GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC 2460
 ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC 2520
 TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG 2580
 CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA 2640
 GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C 2691

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
 1 5 10 15
 Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Pro Glu Lys Thr Pro Ala
 20 25 30
 Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
 35 40 45
 Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
 50 55 60
 Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
 65 70 75 80
 Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
 85 90 95
 Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
 100 105 110
 Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
 115 120 125
 Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
 130 135 140
 Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
 145 150 155 160
 Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
 165 170 175
 Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
 180 185 190
 Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
 195 200 205
 Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
 210 215 220
 Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
 225 230 235 240
 Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
 245 250 255
 Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
 260 265 270
 Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
 275 280 285

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Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Cys	Phe	Ile	Ala	Thr
290						295					300				
Arg	Ile	Gly	Cys	Gln	Gln	Leu	Lys	Ala	Arg	Gly	Glu	Val	Asp	Ile	Leu
305					310					315					320
Gly	Ile	Val	Cys	Gln	Leu	Arg	Leu	Asp	Arg	Gly	Gly	Met	Ile	Gln	Thr
				325					330					335	
Asp	Glu	Gln	Tyr	Gln	Phe	Leu	His	His	Thr	Leu	Ala	Leu	Tyr	Ala	Gly
			340					345					350		
Gln	Leu	Pro	Glu	Glu	Pro	Ser	Pro								
		355					360								

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